

SEQUENCE LISTING

<110> SAKANO, SEIJI
 ITOH, AKIRA

<120> DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

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<140> 09/068,740

<141> 1998-06-18

<150> JP 7-299611

<151> 1995-11-17

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<151> 1995-11-30

<150> PCT/JP96/03356

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Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly Ser Ala Val Thr Pro
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Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp Gly Gly Gly Ala Asp
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Pro	Gly	Trp	Lys	Gly	Pro	Tyr	Cys	Thr	Glu	Pro	Ile	Cys	Leu	Pro	Gly	195	200	205
Cys	Asp	Glu	Gln	His	Gly	Phe	Cys	Asp	Lys	Pro	Gly	Glu	Cys	Lys	Cys	210	215	220
Arg	Val	Gly	Trp	Gln	Gly	Arg	Tyr	Cys	Asp	Glu	Cys	Ile	Arg	Tyr	Pro	225	230	235
Gly	Cys	Leu	His	Gly	Thr	Cys	Gln	Gln	Pro	Trp	Gln	Cys	Asn	Cys	Gln	245	250	255
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Pro	Cys	Phe	Asn	Gly	Gly	Arg	Cys	Ser	Asp	Ser	Pro	Asp	Gly	Gly	Tyr	355	360	365
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Ile	Asp	Tyr	Cys	Ser	Ser	Ser	Pro	Cys	Ser	Asn	Gly	Ala	Lys	Cys	Val	385	390	395
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Pro	Pro	Gly	Tyr	Thr	Gly	Arg	Asn	Cys	Ser	Ala	Pro	Val	Ser	Arg	Cys	450	455	460

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 Trp Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His
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Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His Pro Cys Thr	
920 925 930	
ggt gtg ggc gag tgt cgg tct tcc agt ctc cag ccg gtg aag aca aag	3249
Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val Lys Thr Lys	
935 940 945	

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tgc acc tct gac tcc tat tac cag gat aac tgt gcg aac atc aca ttt	3297
Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn Ile Thr Phe	
950 955 960	
acc ttt aac aag gag atg atg tca cca ggt ctt act acg gag cac att	3345
Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr Glu His Ile	
965 970 975	
tgc agt gaa ttg agg aat ttg aat att ttg aag aat gtt tcc gct gaa	3393
Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val Ser Ala Glu	
980 985 990 995	
tat tca atc tac atc gct tgc gag cct tcc cct tca gcg aac aat gaa	3441
Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala Asn Asn Glu	
1000 1005 1010	
ata cat gtg gcc att tct gct gaa gat ata cgg gat gat ggg aac ccg	3489
Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp Gly Asn Pro	
1015 1020 1025	
atc aag gaa atc act gac aaa ata atc gat ctt gtt agt aaa cgt gat	3537
Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser Lys Arg Asp	
1030 1035 1040	
gga aac agc tcg ctg att gct gcc gtt gca gaa gta aga gtt cag agg	3585
Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg Val Gln Arg	
1045 1050 1055	
cgg cct ctg aag aac aga aca gat ttc ctt gtt ccc ttg ctg agc tct	3633
Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu Leu Ser Ser	
1060 1065 1070 1075	
gtc tta act gtg gct tgg atc tgt tgc ttg gtg acg gcc ttc tac tgg	3681
Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp	
1080 1085 1090	
tgc ctg cgg aag cgg cgg aag ccg ggc agc cac aca cac tca gcc tct	3729
Cys Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr His Ser Ala Ser	
1095 1100 1105	
gag gac aac acc acc aac aac gtg cgg gag cag ctg aac cag atc aaa	3777
Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu Asn Gln Ile Lys	
1110 1115 1120	
aac ccc att gag aaa cat ggg gcc aac acg gtc ccc atc aag gat tat	3825
Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile Lys Asp Tyr	
1125 1130 1135	
gag aac aag aac tcc aaa atg tct aaa ata agg aca cac aat tct gaa	3873
Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His Asn Ser Glu	
1140 1145 1150 1155	
gta gaa gag gac gac atg gac aaa cac cag cag aaa gcc cgg ttt gcc	3921
Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys Ala Arg Phe Ala	
1160 1165 1170	

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aag cag ccg gcg tac acg ctg gta gac aga gaa gag aag ccc ccc aac 3969
 Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu Glu Lys Pro Pro Asn
 1175 1180 1185

ggc acg ccg aca aaa cac cca aac tgg aca aac aaa cag gac aac aga 4017
 Gly Thr Pro Thr Lys His Pro Asn Trp Thr Asn Lys Gln Asp Asn Arg
 1190 1195 1200

gac ttg gaa agt gcc cag agc tta aac cga atg gag tac atc gta 4062
 Asp Leu Glu Ser Ala Gln Ser Leu Asn Arg Met Glu Tyr Ile Val
 1205 1210 1215

tagcagaccg cgggcactgc cgccgctagg tagagtctga gggcttgtag ttctttaaac 4122

tgctgtgtca tactcgagtc tgaggccggt gctgacttag aatccctgtg ttaatttaag 4182

ttttgacaag ctggcttaca ctggca 4208

<210> 11
 <211> 1218
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Arg Ser Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu
 1 5 10 15

Leu Leu Ala Leu Leu Cys Ala Leu Arg Ala Lys Val Cys Gly Ala Ser
 20 25 30

Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu
 35 40 45

Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg
 50 55 60

Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys
 65 70 75 80

Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser
 85 90 95

Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser
 100 105 110

Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp
 115 120 125

Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp
 130 135 140

Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met
 145 150 155 160

Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
 165 170 175

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Ala	His	Phe	Glu	Tyr	Gln	Ile	Arg	Val	Thr	Cys	Asp	Asp	Tyr	Tyr	Tyr	
			180					185					190			
Gly	Phe	Gly	Cys	Asn	Lys	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Phe	Phe	Gly	
		195					200					205				
His	Tyr	Ala	Cys	Asp	Gln	Asn	Gly	Asn	Lys	Thr	Cys	Met	Glu	Gly	Trp	
	210					215					220					
Met	Gly	Pro	Glu	Cys	Asn	Arg	Ala	Ile	Cys	Arg	Gln	Gly	Cys	Ser	Pro	
225					230					235					240	
Lys	His	Gly	Ser	Cys	Lys	Leu	Pro	Gly	Asp	Cys	Arg	Cys	Gln	Tyr	Gly	
				245					250					255		
Trp	Gln	Gly	Leu	Tyr	Cys	Asp	Lys	Cys	Ile	Pro	His	Pro	Gly	Cys	Val	
			260					265					270			
His	Gly	Ile	Cys	Asn	Glu	Pro	Trp	Gln	Cys	Leu	Cys	Glu	Thr	Asn	Trp	
		275					280					285				
Gly	Gly	Gln	Leu	Cys	Asp	Lys	Asp	Leu	Asn	Tyr	Cys	Gly	Thr	His	Gln	
	290					295					300					
Pro	Cys	Leu	Asn	Gly	Gly	Thr	Cys	Ser	Asn	Thr	Gly	Pro	Asp	Lys	Tyr	
305					310					315					320	
Gln	Cys	Ser	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	Pro	Asn	Cys	Glu	Ile	Ala	
				325					330					335		
Glu	His	Ala	Cys	Leu	Ser	Asp	Pro	Cys	His	Asn	Arg	Gly	Ser	Cys	Lys	
			340					345					350			
Glu	Thr	Ser	Leu	Gly	Phe	Glu	Cys	Glu	Cys	Ser	Pro	Gly	Trp	Thr	Gly	
		355					360					365				
Pro	Thr	Cys	Ser	Thr	Asn	Ile	Asp	Asp	Cys	Ser	Pro	Asn	Asn	Cys	Ser	
	370					375						380				
His	Gly	Gly	Thr	Cys	Gln	Asp	Leu	Val	Asn	Gly	Phe	Lys	Cys	Val	Cys	
385					390					395					400	
Pro	Pro	Gln	Trp	Thr	Gly	Lys	Thr	Cys	Gln	Leu	Asp	Ala	Asn	Glu	Cys	
				405					410					415		
Glu	Ala	Lys	Pro	Cys	Val	Asn	Ala	Lys	Ser	Cys	Lys	Asn	Leu	Ile	Ala	
			420					425					430			
Ser	Tyr	Tyr	Cys	Asp	Cys	Leu	Pro	Gly	Trp	Met	Gly	Gln	Asn	Cys	Asp	
		435					440					445				
Ile	Asn	Ile	Asn	Asp	Cys	Leu	Gly	Gln	Cys	Gln	Asn	Asp	Ala	Ser	Cys	
	450					455					460					
Arg	Asp	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Ile	Cys	Pro	Pro	Gly	Tyr	Ala	
465					470					475					480	

Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys
 485 490 495
 Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu
 500 505 510
 Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr
 515 520 525
 Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala
 530 535 540
 Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys
 545 550 555 560
 Ser His Leu Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile Asp
 565 570 575
 Ser Cys Thr Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val Arg
 580 585 590
 Tyr Ile Ser Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser Gln
 595 600 605
 Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr
 610 615 620
 Tyr Cys His Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn
 625 630 635 640
 Gly Gly Thr Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser
 645 650 655
 Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser
 660 665 670
 Gln Asn Pro Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn Asp
 675 680 685
 Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His Ser
 690 695 700
 Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys
 705 710 715 720
 Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp Glu
 725 730 735
 Gly Thr Thr Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn Pro
 740 745 750
 Cys His Asn Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr Cys
 755 760 765
 Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr Asn
 770 775 780

0995593 11900
 10627 2555660

Asp Cys Ser Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly
 785 790 795 800
 Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp
 805 810 815
 Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly
 820 825 830
 Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro
 835 840 845
 Gly His Ser Gly Ala Lys Cys Gln Glu Val Ser Gly Arg Pro Cys Ile
 850 855 860
 Thr Met Gly Ser Val Ile Pro Asp Gly Ala Lys Trp Asp Asp Asp Cys
 865 870 875 880
 Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile Ala Cys Ser Lys Val Trp
 885 890 895
 Cys Gly Pro Arg Pro Cys Leu Leu His Lys Gly His Ser Glu Cys Pro
 900 905 910
 Ser Gly Gln Ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His
 915 920 925
 Pro Cys Thr Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val
 930 935 940
 Lys Thr Lys Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn
 945 950 955 960
 Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr Thr
 965 970 975
 Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys Asn Val
 980 985 990
 Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala
 995 1000 1005
 Asn Asn Glu Ile His Val Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp
 1010 1015 1020
 Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys Ile Ile Asp Leu Val Ser
 1025 1030 1035 1040
 Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala Ala Val Ala Glu Val Arg
 1045 1050 1055
 Val Gln Arg Arg Pro Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu
 1060 1065 1070
 Leu Ser Ser Val Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala
 1075 1080 1085

00005593 112904
 00005593 112904

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<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```



```
<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence
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```
<400> 14
tggcartgya aytgycarga                20
```

```
<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

```
<400> 15
atyttytyt crcarttraa                                     20
```

```
<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

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<220>  
<221> modified_base  
<222> (12)  
<223> a, t, c, g, other or unknown
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<400> 16	
tgcststgyg anaccaactg	20

```
<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence
```

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<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

20

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<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

25

```
<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
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25

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<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
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28

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<220>
<223> Description of Artificial Sequence: Chemical
      Synthesis
```

28

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<210> 22
<211> 55
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<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 22
 tcatttatca tcatcatctt tataatcccc gccctggccc tctagcttct cagtg 55

<210> 23
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 23
 aaccatcccc gaggggtgtct gctggaagcc aggtca 37

<210> 24
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 24
 cctctagagt cgcggccgtc gcactcattt acc 33

<210> 25
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Chemical
 Synthesis

<400> 25
 aaggatcccc gccctggccc tctagcttc 29

<210> 26
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Chemical
 Synthesis

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 T0621T E0556660

<400> 26
cctctagacg cgtagagcgg ccgccaccgc ggtgga

36

<210> 27
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 27
tcacacctca gttgctatga cgcac

25

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 28
ggacgcgtgg atccactagt tctagagc

28

<210> 29
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 29
tcatttatca tcatcatctt tataatccac ctgagttgct atgacgcact c

51

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 30
cggcgcagcg atgcgttccc cacgg

25

0999593 12904
T062T E655660

25

27

28

51

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 35

aaggatccgt tctgttggtc agaggccgcc t

31

<210> 36

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 36

cctctagacg cgtagagcgg ccgccaccgc ggtgga

36

<210> 37

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 37

ctatacgatg tactccattc ggtttaag

28

<210> 38

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 38

ggacgcgtct agatcgacc tgcaggcatg c

31

<210> 39

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemical
Synthesis

<400> 39

ctatttatca tcatcatctt tataatctac gatgtactcc attcggttta ag

52

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<210> 40
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus

<220>
 <221> MOD_RES
 <222> (1)..(45)
 <223> "Xaa" represents a variable amino acid

<400> 40
 Xaa Xaa Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
 1 5 10 15

Arg Pro Arg Asp Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly
 20 25 30

Xaa Xaa Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys
 35 40 45

<210> 41
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 41
 Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
 20 25 30

Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys
 35 40 45

<210> 42
 <211> 45
 <212> PRT
 <213> Drosophila sp.

<400> 42
 Val Thr Cys Asp Leu Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly
 20 25 30

Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp Tyr Cys
 35 40 45

<210> 43

00005593 112901

```

<400> 46
Val Thr Cys Asp Asp Tyr Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
  1                               5          10          15

Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
          20          25          30

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Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro Glu Cys
 35 40 45

<210> 47

<211> 45

<212> PRT

<213> Drosophila sp.

<400> 47

Val Gln Cys Ala Val Thr Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Gln Phe Gly His Tyr Ala Cys Gly Ser Glu Gly
 20 25 30

Gln Lys Leu Cys Leu Asn Gly Trp Gln Gly Val Asn Cys
 35 40 45

<210> 48

<211> 45

<212> PRT

<213> Rattus sp.

<400> 48

Val Thr Cys Asp Asp His Tyr Tyr Gly Phe Gly Cys Asn Lys Phe Cys
 1 5 10 15

Arg Pro Arg Asp Asp Phe Phe Gly His Tyr Ala Cys Asp Gln Asn Gly
 20 25 30

Asn Lys Thr Cys Met Glu Gly Trp Met Gly Pro Glu Cys
 35 40 45

FOOTNOTES: E555555555